

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/987,701

DATE: 12/06/2001
 TIME: 15:06:11

Input Set : A:\es.txt
 Output Set: N:\CRF3\12062001\I987701.raw

#2
 ENTERED

3 <110> APPLICANT: BASCH, Ross S.
 4 ZHANG, Xin-Min
 6 <120> TITLE OF INVENTION: PROTEIN THAT MODULATES THE STABILITY OF TRANSCRIPTIONAL
 REGULATORY
 7 COMPLEXES REGULATING NUCLEAR HORMONE RECEPTOR ACTIVITY, DNA ENCODING SAME, AND
 8 ANTIBODIES THERETO
 10 <130> FILE REFERENCE: BASCH=1A
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/987,701
 13 <141> CURRENT FILING DATE: 2001-11-15
 15 <150> PRIOR APPLICATION NUMBER: 60/248,191
 16 <151> PRIOR FILING DATE: 2000-11-15
 18 <160> NUMBER OF SEQ ID NOS: 17
 20 <170> SOFTWARE: PatentIn version 3.1
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 23 <211> LENGTH: 3885
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
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 29 <222> LOCATION: (161)..(1705)
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 36 <223> OTHER INFORMATION: n is a, c, g or t.
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 48 attggcgggtg accggatatt cagttgcaca tccccacatc aatgcactgc caatggggtta 120
 50 tatcctgtgt tgtgacctca tggtttaagt gggaataaag atg agt ata agc agt 175
 51 Met Ser Ile Ser Ser
 52 1 5
 54 gat gag gtc aac ttc ttg gta tat aga tac ttg caa gag tca gga ttt 223
 55 Asp Glu Val Asn Phe Leu Val Tyr Arg Tyr Leu Gln Glu Ser Gly Phe
 56 10 15 20
 58 tct cat tca gca ttt acc ttt ggt ata aaa agc cat atc agt cag tcc 271
 59 Ser His Ser Ala Phe Thr Phe Gly Ile Lys Ser His Ile Ser Gln Ser
 60 25 30 35
 62 aat ata aat ggt gcc ctc gtc cca ccc gct gca ttg att tct atc atc 319
 63 Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala Leu Ile Ser Ile Ile
 64 40 45 50
 66 cag aaa ggt cta cag tat gta gaa gca gaa gtt agt att aat gag gat 367
 67 Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val Ser Ile Asn Glu Asp
 68 55 60 65
 70 ggt acc ttg ttt gat ggt cga cca ata gag tct ctg tcc ctg ata gat 415

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71 Gly Thr Leu Phe Asp Gly Arg Pro Ile Glu Ser Leu Ser Leu Ile Asp
72 70 75 80 85
74 gcc gta atg cct gat gta gta caa aca aga caa caa gct tat aga gat 463
75 Ala Val Met Pro Asp Val Val Gln Thr Arg Gln Gln Ala Tyr Arg Asp
76 90 95 100
78 aag ctt gca cag caa cag gca gca gct gct gca gct gcc gca gct gca 511
79 Lys Leu Ala Gln Gln Gln Ala Ala Ala Ala Ala Ala Ala Ala Ala
80 105 110 115
82 gcc agc caa caa gga tct gca aaa aat gga gaa aac aca gca aat ggg 559
83 Ala Ser Gln Gln Gly Ser Ala Lys Asn Gly Glu Asn Thr Ala Asn Gly
84 120 125 130
86 gag gag aat gga gca cat act ata gca aat aat cat act gat atg atg 607
87 Glu Glu Asn Gly Ala His Thr Ile Ala Asn Asn His Thr Asp Met Met
88 135 140 145
90 gaa gtg gat ggg gat gtt gaa atc cct cct aat aaa gct gtt gtg ttg 655
91 Glu Val Asp Gly Asp Val Glu Ile Pro Pro Asn Lys Ala Val Val Leu
92 150 155 160 165
94 cgg ggc cat gaa tct gaa gtt ttt atc tgt gcc tgg aac cct gtt agt 703
95 Arg Gly His Glu Ser Glu Val Phe Ile Cys Ala Trp Asn Pro Val Ser
96 170 175 180
98 gat ctc cta gca tca ggg tct gga gac tca aca gca aga ata tgg aat 751
99 Asp Leu Leu Ala Ser Gly Ser Gly Asp Ser Thr Ala Arg Ile Trp Asn
100 185 190 195
102 ctt agt gag aac agc acc agt ggc tct aca cag tta gta ctt aga cat 799
103 Leu Ser Glu Asn Ser Thr Ser Gly Ser Thr Gln Leu Val Leu Arg His
104 200 205 210
106 tgt ata cga gaa gga ggg caa gat gtt ccg agc aac aag gat gtc aca 847
107 Cys Ile Arg Glu Gly Gly Gln Asp Val Pro Ser Asn Lys Asp Val Thr
108 215 220 225
110 tct cta gat tgg aat agt gaa ggt aca ctt cta gca act ggt tcc tat 895
111 Ser Leu Asp Trp Asn Ser Glu Gly Thr Leu Leu Ala Thr Gly Ser Tyr
112 230 235 240 245
114 gat ggg ttt gcc aga ata tgg act aaa gat ggt aac ctt gct agc acc 943
115 Asp Gly Phe Ala Arg Ile Trp Thr Lys Asp Gly Asn Leu Ala Ser Thr
116 250 255 260
118 tta ggg cag cat aaa ggc cct ata ttt gca tta aaa tgg aat aag aaa 991
119 Leu Gly Gln His Lys Gly Pro Ile Phe Ala Leu Lys Trp Asn Lys Lys
120 265 270 275
122 gga aat ttc atc cta agt gct gga gta gac aag act aca att att tgg 1039
123 Gly Asn Phe Ile Leu Ser Ala Gly Val Asp Lys Thr Thr Ile Ile Trp
124 280 285 290
126 gac gca cat act ggt gaa gcc aag caa cag ttt cct ttt cat tca gca 1087
127 Asp Ala His Thr Gly Glu Ala Lys Gln Gln Phe Pro Phe His Ser Ala
128 295 300 305
130 cca gca ttg gat gtt gat tgg cag agc aac aac acc ttt gct tct tgt 1135
131 Pro Ala Leu Asp Val Asp Trp Gln Ser Asn Asn Thr Phe Ala Ser Cys
132 310 315 320 325
134 agt aca gat atg tgc att cat gtc tgt aaa tta gga caa gac aga cct 1183
135 Ser Thr Asp Met Cys Ile His Val Cys Lys Leu Gly Gln Asp Arg Pro

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136		330		335		340	
138	att aaa aca ttc caa gga cat acg aat gaa gta aat gct atc aaa tgg						1231
139	Ile Lys Thr Phe Gln Gly His Thr Asn Glu Val Asn Ala Ile Lys Trp						
140		345		350		355	
142	gac cca act ggc aat ctc ttg gcc tcc tgt tct gac gac atg act tta						1279
143	Asp Pro Thr Gly Asn Leu Leu Ala Ser Cys Ser Asp Asp Met Thr Leu						
144		360		365		370	
146	aag ata tgg agt atg aaa caa gac aat tgt gtc cat gat ttg cag caa						1327
147	Lys Ile Trp Ser Met Lys Gln Asp Asn Cys Val His Asp Leu Gln Gln						
148		375		380		385	
150	cat aat aaa gaa att tat act atc aaa tgg agt cca aca gga cca ggg						1375
151	His Asn Lys Glu Ile Tyr Thr Ile Lys Trp Ser Pro Thr Gly Pro Gly						
152	390		395		400		405
154	act aat aat cca aat gcc aac ctt atg tta gca agt gca tcc ttt gat						1423
155	Thr Asn Asn Pro Asn Ala Asn Leu Met Leu Ala Ser Ala Ser Phe Asp						
156		410		415		420	
158	tct act gtt agg tta tgg gat gta gac cga ggg ata tgc atc cat acc						1471
159	Ser Thr Val Arg Leu Trp Asp Val Asp Arg Gly Ile Cys Ile His Thr						
160		425		430		435	
162	ttg aca aaa cac caa gag cct gtg tac agt gta gct ttc agt cct gat						1519
163	Leu Thr Lys His Gln Glu Pro Val Tyr Ser Val Ala Phe Ser Pro Asp						
164		440		445		450	
166	ggc agg tat ctg gca agt ggt tct ttt gac aaa tgt gta cac atc tgg						1567
167	Gly Arg Tyr Leu Ala Ser Gly Ser Phe Asp Lys Cys Val His Ile Trp						
168		455		460		465	
170	aac acg cag aca ggt gct cta gtt cac agc tat agg gga aca ggt gga						1615
171	Asn Thr Gln Thr Gly Ala Leu Val His Ser Tyr Arg Gly Thr Gly Gly						
172		470		475		480	
174	ata ttt gaa gtt tgc tgg aat gca gca gga gac aaa gtt gga gcc agt						1663
175	Ile Phe Glu Val Cys Trp Asn Ala Ala Gly Asp Lys Val Gly Ala Ser						
176		490		495		500	
178	gca tca gat ggt tca gtt tgt gta tta gac ctt cgg aaa tag						1705
179	Ala Ser Asp Gly Ser Val Cys Val Leu Asp Leu Arg Lys						
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182	cgctactagt tggagccat ggaccgacta tgaatgtgta catagccaaa atgagtgtcc						1765
184	ctgacccatg taatgttata gtcccacttg aaccatggcc agtccaatac agccaaatct						1825
186	aaaagaaata tatacataca gtgtatataa acaaaattac accctgaaga tgacagagtt						1885
188	ttgtcacagc ttgtgaattc tgttcaccaa gtgctggaat ctaatctgct gtgcccctaa						1945
190	aatagcattt agaagttttg gatatgaaaa acagaagaga gaaaatatac attataaaaag						2005
192	cagtacatac atgtaccagt ttttggatac taaatgacag ccttgtttct cccctttgaa						2065
194	tcagcagaca ccatggatta tattcttttt ttcccttcag tagtgagcag tttgtatgta						2125
196	cagagaaaaat ggacttacaa aaacttgcag cagtagtttg ttcttgcttt aaaatttcgt						2185
198	ttttggttta gattatggat gcatgaagta agggagtgaa tcagtttctt gtttatattt						2245
200	ttttcacctt ttaacaaaaa aattctttta aatattttta tgcattcttt tgaagaggta						2305
202	gatgttttgt acattttatg gctcccagag catatatcca gttggtgcat gttgtggaag						2365
204	ggggaatttg aaattaaatg gaaaacctat gacttttggtc ctgtcaatct gtaagacaca						2425
206	tcagtaaaaa ggtattatgc tctgttggtt ttgttttttt gttttgcttt tttttttttt						2485
208	tttttttttg ttttttggtg atgtggctta aatgcaatag tttttttttt gggacatatt						2545
210	tctgccattt aaagactaga agggcacacac ttttttttta attaccatag agaagatata						2605

WOK

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 216 ttaagagatt aaaatgtttc tggataagga ttagcttctc gaagtgtoca tcattctgtg 2785
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 220 ctttatacaa agcaagataa cggcatataa cactgccatt acatggcaaa atgtttgcta 2905
 222 ccttagttta aaaaacaatc tcaaacaaaa gacttgcttc aagggtgtttt taaatagcag 2965
 224 tgattcagaa ttttttttaa tgaaagtata attgcaactaa ccttcttctc gctgctctga 3025
 226 ttctgcattt gtggtacttg tgactacgtt ttttcaaata tagatagatt taagctgcta 3085
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 230 gtattttctt aaagatatag atattaaacc ttgtgctcat gcaacttaga gtaacatata 3205
 232 cagacaaatg attgcatgag gccatgttta tatgtgtgac taataaggct tgctcatgatt 3265
 234 aacataatcc aggtatgtca tttctgaaga gaatagtcac caaatttata tctcgaagat 3325
 236 ttttaattaag ggaattgctt attgtttgag cttagcaaat taataacact atttctgtca 3385
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 244 taaagagaat aaatacactt aatttcacaa tacattgtta tatgtacccc agttgttggt 3625
 246 agtggggact atgatactgt aataatattt ttaaaaattt acatcaagag aggcagtcac 3685
 248 tcacgatggg tttgtgccag ctcttttttag ggttttggat cacattagag atatttagaa 3745
 250 catattaccc tgtgacttac gtaggaaacc taatatgctg agtatctggc acttgaattc 3805
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 254 aaaaaaaaaa aaaaaaaaaa 3885
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 258 <211> LENGTH: 514
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 273 His Ile Ser Gln Ser Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala
 274 35 40 45
 277 Leu Ile Ser Ile Ile Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val
 278 50 55 60
 281 Ser Ile Asn Glu Asp Gly Thr Leu Phe Asp Gly Arg Pro Ile Glu Ser
 282 65 70 75 80
 285 Leu Ser Leu Ile Asp Ala Val Met Pro Asp Val Val Gln Thr Arg Gln
 286 85 90 95
 289 Gln Ala Tyr Arg Asp Lys Leu Ala Gln Gln Gln Ala Ala Ala Ala
 290 100 105 110
 293 Ala Ala Ala Ala Ala Ser Gln Gly Ser Ala Lys Asn Gly Glu
 294 115 120 125
 297 Asn Thr Ala Asn Gly Glu Glu Asn Gly Ala His Thr Ile Ala Asn Asn
 298 130 135 140
 301 His Thr Asp Met Met Glu Val Asp Gly Asp Val Glu Ile Pro Pro Asn
 302 145 150 155 160
 305 Lys Ala Val Val Leu Arg Gly His Glu Ser Glu Val Phe Ile Cys Ala

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306          165          170          175
309 Trp Asn Pro Val Ser Asp Leu Leu Ala Ser Gly Ser Gly Asp Ser Thr
310          180          185          190
313 Ala Arg Ile Trp Asn Leu Ser Glu Asn Ser Thr Ser Gly Ser Thr Gln
314          195          200          205
317 Leu Val Leu Arg His Cys Ile Arg Glu Gly Gly Gln Asp Val Pro Ser
318          210          215          220
321 Asn Lys Asp Val Thr Ser Leu Asp Trp Asn Ser Glu Gly Thr Leu Leu
322 225          230          235          240
325 Ala Thr Gly Ser Tyr Asp Gly Phe Ala Arg Ile Trp Thr Lys Asp Gly
326          245          250          255
329 Asn Leu Ala Ser Thr Leu Gly Gln His Lys Gly Pro Ile Phe Ala Leu
330          260          265          270
333 Lys Trp Asn Lys Lys Gly Asn Phe Ile Leu Ser Ala Gly Val Asp Lys
334          275          280          285
337 Thr Thr Ile Ile Trp Asp Ala His Thr Gly Glu Ala Lys Gln Gln Phe
338          290          295          300
341 Pro Phe His Ser Ala Pro Ala Leu Asp Val Asp Trp Gln Ser Asn Asn
342 305          310          315          320
345 Thr Phe Ala Ser Cys Ser Thr Asp Met Cys Ile His Val Cys Lys Leu
346          325          330          335
349 Gly Gln Asp Arg Pro Ile Lys Thr Phe Gln Gly His Thr Asn Glu Val
350          340          345          350
353 Asn Ala Ile Lys Trp Asp Pro Thr Gly Asn Leu Leu Ala Ser Cys Ser
354          355          360          365
357 Asp Asp Met Thr Leu Lys Ile Trp Ser Met Lys Gln Asp Asn Cys Val
358          370          375          380
361 His Asp Leu Gln Gln His Asn Lys Glu Ile Tyr Thr Ile Lys Trp Ser
362 385          390          395          400
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366          405          410          415
369 Ser Ala Ser Phe Asp Ser Thr Val Arg Leu Trp Asp Val Asp Arg Gly
370          420          425          430
373 Ile Cys Ile His Thr Leu Thr Lys His Gln Glu Pro Val Tyr Ser Val
374          435          440          445
377 Ala Phe Ser Pro Asp Gly Arg Tyr Leu Ala Ser Gly Ser Phe Asp Lys
378          450          455          460
381 Cys Val His Ile Trp Asn Thr Gln Thr Gly Ala Leu Val His Ser Tyr
382 465          470          475          480
385 Arg Gly Thr Gly Gly Ile Phe Glu Val Cys Trp Asn Ala Ala Gly Asp
386          485          490          495
389 Lys Val Gly Ala Ser Ala Ser Asp Gly Ser Val Cys Val Leu Asp Leu
390          500          505          510
393 Arg Lys
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398 <211> LENGTH: 2078
399 <212> TYPE: DNA
400 <213> ORGANISM: Homo sapiens
402 <220> FEATURE:

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VERIFICATION SUMMARY

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Input Set : A:\es.txt

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L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:218 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:263 M:283 W: Missing Blank Line separator, <400> field identifier